

SEQUENCE LISTING

<110> Xu, Haiyan
Chen, Hong
Barnes, Glenn

<120> METHODS AND COMPOSITIONS FOR USE OF
INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
METABOLIC DISORDERS

<130> MPI2003-025P1RNM

<150> 60/446041

<151> 2003-02-07

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1449

<212> DNA

<213> human

<220>

<221> CDS

<222> (1)...(1449)

<400> 1

atg gcg tct ttc tct gct gag acc aat tca act gac cta ctc tca cag	48
Met Ala Ser Phe Ser Ala Glu Thr Asn Ser Thr Asp Leu Leu Ser Gln	
1 5 10 15	
cca tgg aat gag ccc cca gta att ctc tcc atg gtc att ctc agc ctt	96
Pro Trp Asn Glu Pro Pro Val Ile Leu Ser Met Val Ile Leu Ser Leu	
20 25 30	
act ttt tta ctg gga ttg cca ggc aat ggg ctg gtg ctg tgg gtg gct	144
Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala	
35 40 45	
ggc ctg aag atg cag cgg aca gtg aac aca att tgg ttc ctc cac ctc	192
Gly Leu Lys Met Gln Arg Thr Val Asn Thr Ile Trp Phe Leu His Leu	
50 55 60	
acc ttg gcg gac ctc ctc tgc tgc ctc tcc ttg ccc ttc tcg ctg gct	240
Thr Leu Ala Asp Leu Leu Cys Cys Leu Ser Leu Pro Phe Ser Leu Ala	
65 70 75 80	
cac ttg gct ctc cag gga cag tgg ccc tac ggc agg ttc cta tgc aag	288
His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys	
85 90 95	
ctc atc ccc tcc atc att gtc ctc aac atg ttt gcc agt gtc ttc ctg	336
Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Ala Ser Val Phe Leu	
100 105 110	
ctt act gcc att agc ctg gat cgc tgt ctt gtg gta ttc aag cca atc	384
Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile	
115 120 125	
tgg tgt cag aat cat cgc aat gta ggg atg gcc tgc tct atc tgt gga	432
Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly	
130 135 140	
tgt atc tgg gtg gtg gct ttt gtg atg tgc att cct gtg ttc gtg tac	480
Cys Ile Trp Val Val Ala Phe Val Met Cys Ile Pro Val Phe Val Tyr	
145 150 155 160	

cgg gaa atc ttc act aca gac aac cat aat aga tgt ggc tac aaa ttt	528
Arg Glu Ile Phe Thr 165 Thr Asp Asn His Asn 170 Arg Cys Gly Tyr Lys Phe	
ggt ctc tcc agc tca tta gat tat cca gac ttt tat gga gat cca cta	576
Gly Leu Ser Ser 180 Ser Leu Asp Tyr Pro 185 Asp Phe Tyr Gly Asp Pro Leu	
gaa aac agg tct ctt gaa aac att gtt cag ccg cct gga gaa atg aat	624
Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn	
gat agg tta gat cct tcc tct ttc caa aca aat gat cat cct tgg aca	672
Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr	
gtc ccc act gtc ttc caa cct caa aca ttt caa aga cct tct gca gat	720
Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp	
tca ctc cct agg ggt tct gct agg tta aca agt caa aat ctg tat tct	768
Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser	
aat gta ttt aaa cct gct gat gtg gtc tca cct aaa atc ccc agt ggg	816
Asn Val Phe Lys 260 Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly	
ttt cct att gaa gat cac gaa acc agc cca ctg gat aac tct gat gct	864
Phe Pro Ile Glu Asp His Glu Thr 280 Pro Leu Asp Asn Ser Asp Ala	
ttt ctc tct act cat tta aag ctg ttc cct agc gct tct agc aat tcc	912
Phe Leu Ser Thr His Leu Lys 295 Leu Phe Pro Ser Ala Ser Ser Asn Ser	
ttc tac gag tct gag cta cca caa ggt ttc cag gat tat tac aat tta	960
Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu	
ggc caa ttc aca gat gac gat caa gtg cca aca ccc ctc gtg gca ata	1008
Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile	
acg atc act agg cta gtg gtg ggt ttc ctg ctg ccc tct gtt atc atg	1056
Thr Ile Thr Arg Leu Val Val Gly Phe 345 Leu Leu Pro Ser Val Ile Met	
ata gcc tgt tac agc ttc att gtc ttc cga atg caa agg ggc cgc ttc	1104
Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe	
gcc aag tct cag agc aaa acc ttt cga gtg gcc gtg gtg gtg gct	1152
Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Val Ala	
gtc ttt ctt gtc tgc tgg act cca tac cac att ttt gga gtc ctg tca	1200
Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Phe Gly Val Leu Ser	
ttg ctt act gac cca gaa act ccc ttg ggg aaa act ctg atg tcc tgg	1248
Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp	
gat cat gta tgc att gct cta gca tct gcc aat agt tgc ttt aat ccc	1296
Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro	

ttc	ctt	tat	gcc	ctc	ttg	ggg	aaa	gat	ttt	agg	aag	aaa	gca	agg	cag	1344
Phe	Leu	Tyr	Ala	Leu	Leu	Gly	Lys	Asp	Phe	Arg	Lys	Lys	Ala	Arg	Gln	
		435					440					445				
tcc	att	cag	gga	att	ctg	gag	gca	gcc	ttc	agt	gag	gag	ctc	aca	cgt	1392
Ser	Ile	Gln	Gly	Ile	Leu	Glu	Ala	Ala	Phe	Ser	Glu	Glu	Leu	Thr	Arg	
	450					455					460					
tcc	acc	cac	tgt	ccc	tca	aac	aat	gtc	att	tca	gaa	aga	aat	agt	aca	1440
Ser	Thr	His	Cys	Pro	Ser	Asn	Asn	Val	Ile	Ser	Glu	Arg	Asn	Ser	Thr	
465					470					475					480	
act	gtg	tga														1449
Thr	Val	*														

<210> 2
 <211> 482
 <212> PRT
 <213> human

<400> 2

Met	Ala	Ser	Phe	Ser	Ala	Glu	Thr	Asn	Ser	Thr	Asp	Leu	Leu	Ser	Gln
1				5					10					15	
Pro	Trp	Asn	Glu	Pro	Pro	Val	Ile	Leu	Ser	Met	Val	Ile	Leu	Ser	Leu
		20						25					30		
Thr	Phe	Leu	Leu	Gly	Leu	Pro	Gly	Asn	Gly	Leu	Val	Leu	Trp	Val	Ala
	35						40				45				
Gly	Leu	Lys	Met	Gln	Arg	Thr	Val	Asn	Thr	Ile	Trp	Phe	Leu	His	Leu
	50					55					60				
Thr	Leu	Ala	Asp	Leu	Leu	Cys	Cys	Leu	Ser	Leu	Pro	Phe	Ser	Leu	Ala
65				70						75					80
His	Leu	Ala	Leu	Gln	Gly	Gln	Trp	Pro	Tyr	Gly	Arg	Phe	Leu	Cys	Lys
			85						90					95	
Leu	Ile	Pro	Ser	Ile	Ile	Val	Leu	Asn	Met	Phe	Ala	Ser	Val	Phe	Leu
		100						105					110		
Leu	Thr	Ala	Ile	Ser	Leu	Asp	Arg	Cys	Leu	Val	Val	Phe	Lys	Pro	Ile
	115						120				125				
Trp	Cys	Gln	Asn	His	Arg	Asn	Val	Gly	Met	Ala	Cys	Ser	Ile	Cys	Gly
	130					135					140				
Cys	Ile	Trp	Val	Val	Ala	Phe	Val	Met	Cys	Ile	Pro	Val	Phe	Val	Tyr
145					150					155					160
Arg	Glu	Ile	Phe	Thr	Thr	Asp	Asn	His	Asn	Arg	Cys	Gly	Tyr	Lys	Phe
			165						170					175	
Gly	Leu	Ser	Ser	Ser	Leu	Asp	Tyr	Pro	Asp	Phe	Tyr	Gly	Asp	Pro	Leu
		180						185					190		
Glu	Asn	Arg	Ser	Leu	Glu	Asn	Ile	Val	Gln	Pro	Pro	Gly	Glu	Met	Asn
	195						200					205			
Asp	Arg	Leu	Asp	Pro	Ser	Ser	Phe	Gln	Thr	Asn	Asp	His	Pro	Trp	Thr
	210					215					220				
Val	Pro	Thr	Val	Phe	Gln	Pro	Gln	Thr	Phe	Gln	Arg	Pro	Ser	Ala	Asp
225					230					235					240
Ser	Leu	Pro	Arg	Gly	Ser	Ala	Arg	Leu	Thr	Ser	Gln	Asn	Leu	Tyr	Ser
			245						250					255	
Asn	Val	Phe	Lys	Pro	Ala	Asp	Val	Val	Ser	Pro	Lys	Ile	Pro	Ser	Gly
		260						265					270		
Phe	Pro	Ile	Glu	Asp	His	Glu	Thr	Ser	Pro	Leu	Asp	Asn	Ser	Asp	Ala
		275					280					285			
Phe	Leu	Ser	Thr	His	Leu	Lys	Leu	Phe	Pro	Ser	Ala	Ser	Ser	Asn	Ser
	290					295					300				
Phe	Tyr	Glu	Ser	Glu	Leu	Pro	Gln	Gly	Phe	Gln	Asp	Tyr	Tyr	Asn	Leu
	305				310					315					320
Gly	Gln	Phe	Thr	Asp	Asp	Asp	Gln	Val	Pro	Thr	Pro	Leu	Val	Ala	Ile
			325						330					335	
Thr	Ile	Thr	Arg	Leu	Val	Val	Gly	Phe	Leu	Leu	Pro	Ser	Val	Ile	Met
			340					345					350		
Ile	Ala	Cys	Tyr	Ser	Phe	Ile	Val	Phe	Arg	Met	Gln	Arg	Gly	Arg	Phe
		355					360					365			

Trp	Gly	Leu	Ala	Leu	Leu	Leu	Thr	Ile	Pro	Ser	Phe	Leu	Tyr	Arg	Val		
				165					170					175			
gtc	cgg	gag	gag	tac	ttt	cca	cca	aag	gtg	ttg	tgt	ggc	gtg	gac	tac	576	
Val	Arg	Glu	Glu	Tyr	Phe	Pro	Pro	Lys	Val	Leu	Cys	Gly	Val	Asp	Tyr		
			180					185					190				
agc	cac	gac	aaa	cgg	cgg	gag	cga	gcc	gtg	gcc	atc	gtc	cgg	ctg	gtc	624	
Ser	His	Asp	Lys	Arg	Arg	Glu	Arg	Ala	Val	Ala	Ile	Val	Arg	Leu	Val		
		195					200					205					
ctg	ggc	ttc	ctg	tgg	cct	cta	ctc	acg	ctc	acg	att	tgt	tac	act	ttc	672	
Leu	Gly	Phe	Leu	Trp	Pro	Leu	Leu	Thr	Leu	Thr	Ile	Cys	Tyr	Thr	Phe		
	210					215					220						
atc	ctg	ctc	cgg	acg	tgg	agc	cgc	agg	gcc	acg	cgg	tcc	acc	aag	aca	720	
Ile	Leu	Leu	Arg	Thr	Trp	Ser	Arg	Arg	Ala	Thr	Arg	Ser	Thr	Lys	Thr		
225					230				235						240		
ctc	aag	gtg	gtg	gtg	gca	gtg	gtg	gcc	agt	ttc	ttt	atc	ttc	tgg	ttg	768	
Leu	Lys	Val	Val	Val	Ala	Val	Val	Ala	Ser	Phe	Phe	Ile	Phe	Trp	Leu		
				245				250						255			
ccc	tac	cag	gtg	acg	ggg	ata	atg	atg	tcc	ttc	ctg	gag	cca	tcg	tca	816	
Pro	Tyr	Gln	Val	Thr	Gly	Ile	Met	Met	Ser	Phe	Leu	Glu	Pro	Ser	Ser		
			260					265					270				
ccc	acc	ttc	ctg	ctg	ctg	aat	aag	ctg	gac	tcc	ctg	tgt	gtc	tcc	ttt	864	
Pro	Thr	Phe	Leu	Leu	Leu	Asn	Lys	Leu	Asp	Ser	Leu	Cys	Val	Ser	Phe		
		275					280					285					
gcc	tac	atc	aac	tgc	tgc	atc	aac	ccc	atc	atc	tac	gtg	gtg	gcc	ggc	912	
Ala	Tyr	Ile	Asn	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Val	Val	Ala	Gly		
	290					295					300						
cag	ggc	ttc	cag	ggc	cga	ctg	cgg	aaa	tcc	ctc	ccc	agc	ctc	ctc	cgg	960	
Gln	Gly	Phe	Gln	Gly	Arg	Leu	Arg	Lys	Ser	Leu	Pro	Ser	Leu	Leu	Arg		
305					310					315					320		
aac	gtg	ttg	act	gaa	gag	tcc	gtg	gtt	agg	gag	agc	aag	tca	ttc	acg	1008	
Asn	Val	Leu	Thr	Glu	Glu	Ser	Val	Val	Arg	Glu	Ser	Lys	Ser	Phe	Thr		
				325					330					335			
cgc	tcc	aca	gtg	gac	act	atg	gcc	cag	aag	acc	cag	gca	gtg	tag		1053	
Arg	Ser	Thr	Val	Asp	Thr	Met	Ala	Gln	Lys	Thr	Gln	Ala	Val	*			
			340				345						350				
gcgacacgtc atgggccact gtggcgatgt cccttcctt																1092	
<210> 4																	
<211> 350																	
<212> PRT																	
<213> human																	
<400> 4																	
Met	Asn	Ser	Phe	Asn	Tyr	Thr	Thr	Pro	Asp	Tyr	Gly	His	Tyr	Asp	Asp		
1				5					10					15			
Lys	Asp	Thr	Leu	Asp	Leu	Asn	Thr	Pro	Val	Asp	Lys	Thr	Ser	Asn	Thr		
			20					25					30				
Leu	Arg	Val	Pro	Asp	Ile	Leu	Ala	Leu	Val	Ile	Phe	Ala	Val	Val	Phe		
		35					40				45						
Leu	Val	Gly	Val	Leu	Gly	Asn	Ala	Leu	Val	Val	Trp	Val	Thr	Ala	Phe		
	50					55					60						
Glu	Ala	Lys	Arg	Thr	Ile	Asn	Ala	Ile	Trp	Phe	Leu	Asn	Leu	Ala	Val		
65				70					75						80		
Ala	Asp	Phe	Leu	Ser	Cys	Leu	Ala	Leu	Pro	Ile	Leu	Phe	Thr	Ser	Ile		
				85					90					95			
Val	Gln	His	His	His	Trp	Pro	Phe	Gly	Gly	Ala	Ala	Cys	Ser	Ile	Leu		
			100					105						110			

Pro	Ser	Leu	Ile	Leu	Leu	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	Leu	Ala
		115					120					125			
Thr	Ile	Ser	Ala	Asp	Arg	Phe	Leu	Leu	Val	Phe	Lys	Pro	Ile	Trp	Cys
	130					135					140				
Gln	Asn	Phe	Arg	Gly	Ala	Gly	Leu	Ala	Trp	Ile	Ala	Cys	Ala	Val	Ala
145				150						155					160
Trp	Gly	Leu	Ala	Leu	Leu	Thr	Ile	Pro	Ser	Phe	Leu	Tyr	Arg	Val	
				165				170						175	
Val	Arg	Glu	Glu	Tyr	Phe	Pro	Pro	Lys	Val	Leu	Cys	Gly	Val	Asp	Tyr
		180						185					190		
Ser	His	Asp	Lys	Arg	Arg	Glu	Arg	Ala	Val	Ala	Ile	Val	Arg	Leu	Val
		195					200					205			
Leu	Gly	Phe	Leu	Trp	Pro	Leu	Leu	Thr	Leu	Thr	Ile	Cys	Tyr	Thr	Phe
	210					215					220				
Ile	Leu	Leu	Arg	Thr	Trp	Ser	Arg	Arg	Ala	Thr	Arg	Ser	Thr	Lys	Thr
225				230						235					240
Leu	Lys	Val	Val	Val	Ala	Val	Val	Ala	Ser	Phe	Phe	Ile	Phe	Trp	Leu
				245					250					255	
Pro	Tyr	Gln	Val	Thr	Gly	Ile	Met	Met	Ser	Phe	Leu	Glu	Pro	Ser	Ser
			260					265					270		
Pro	Thr	Phe	Leu	Leu	Leu	Asn	Lys	Leu	Asp	Ser	Leu	Cys	Val	Ser	Phe
		275					280					285			
Ala	Tyr	Ile	Asn	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Val	Val	Ala	Gly
	290					295					300				
Gln	Gly	Phe	Gln	Gly	Arg	Leu	Arg	Lys	Ser	Leu	Pro	Ser	Leu	Leu	Arg
305				310						315					320
Asn	Val	Leu	Thr	Glu	Glu	Ser	Val	Val	Arg	Glu	Ser	Lys	Ser	Phe	Thr
				325					330					335	
Arg	Ser	Thr	Val	Asp	Thr	Met	Ala	Gln	Lys	Thr	Gln	Ala	Val		
			340					345					350		

<210> 5
 <211> 1412
 <212> DNA
 <213> human

<220>
 <221> CDS
 <222> (27) ... (1247)

<400> 5	
ctcttccaga ggcaagacca accaag atg agt gcc ttg gga gct gtc att gcc	53
Met Ser Ala Leu Gly Ala Val Ile Ala	
1 5	
ctc ctg ctc tgg gga cag ctt ttt gca gtg gac tca ggc aat gat gtc	101
Leu Leu Leu Trp Gly Gln Leu Phe Ala Val Asp Ser Gly Asn Asp Val	
10 15 20 25	
acg gat atc gca gat gac ggc tgc ccg aag ccc ccc gag att gca cat	149
Thr Asp Ile Ala Asp Asp Gly Cys Pro Lys Pro Pro Glu Ile Ala His	
30 35 40	
ggc tat gtg gag cac tcg gtt cgc tac cag tgt aag aac tac tac aaa	197
Gly Tyr Val Glu His Ser Val Arg Tyr Gln Cys Lys Asn Tyr Tyr Lys	
45 50 55	
ctg cgc aca gaa gga gat gga gta tac acc tta aat gat aag aag cag	245
Leu Arg Thr Glu Gly Asp Gly Val Tyr Thr Leu Asn Asp Lys Lys Gln	
60 65 70	
tgg ata aat aag gct gtt gga gat aaa ctt cct gaa tgt gaa gca gat	293
Trp Ile Asn Lys Ala Val Gly Asp Lys Leu Pro Glu Cys Glu Ala Asp	
75 80 85	
gac ggc tgc ccg aag ccc ccc gag att gca cat ggc tat gtg gag cac	341
Asp Gly Cys Pro Lys Pro Pro Glu Ile Ala His Gly Tyr Val Glu His	
90 95 100 105	

tcg gtt cgc tac cag tgt aag aac tac tac aaa ctg cgc aca gaa gga	389
Ser Val Arg Tyr Gln Cys Lys Asn Tyr Tyr Lys Leu Arg Thr Glu Gly	
	110 115 120
gat gga gtg tac acc tta aac aat gag aag cag tgg ata aat aag gct	437
Asp Gly Val Tyr Thr Leu Asn Asn Glu Lys Gln Trp Ile Asn Lys Ala	
	125 130 135
gtt gga gat aaa ctt cct gaa tgt gaa gca gta tgt ggg aag ccc aag	485
Val Gly Asp Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys	
	140 145 150
aat ccg gca aac cca gtg cag cgg atc ctg ggt gga cac ctg gat gcc	533
Asn Pro Ala Asn Pro Val Gln Arg Ile Leu Gly Gly His Leu Asp Ala	
	155 160 165
aaa ggc agc ttt ccc tgg cag gct aag atg gtt tcc cac cat aat ctc	581
Lys Gly Ser Phe Pro Trp Gln Ala Lys Met Val Ser His His Asn Leu	
	170 175 180 185
acc aca ggt gcc acg ctg atc aat gaa caa tgg ctg ctg acc acg gct	629
Thr Thr Gly Ala Thr Leu Ile Asn Glu Gln Trp Leu Leu Thr Thr Ala	
	190 195 200
aaa aat ctc ttc ctg aac cat tca gaa aat gca aca gcg aaa gac att	677
Lys Asn Leu Phe Leu Asn His Ser Glu Asn Ala Thr Ala Lys Asp Ile	
	205 210 215
gcc ccc act tta aca ctc tat gtg ggg aaa aag cag ctt gta gag att	725
Ala Pro Thr Leu Thr Leu Tyr Val Gly Lys Lys Gln Leu Val Glu Ile	
	220 225 230
gag aag gtt gtt cta cac cct aac tac tcc caa gta gat att ggg ctc	773
Glu Lys Val Val Leu His Pro Asn Tyr Ser Gln Val Asp Ile Gly Leu	
	235 240 245
atc aaa ctc aaa cag aag gtg tct gtt aat gag aga gtg atg ccc atc	821
Ile Lys Leu Lys Gln Lys Val Ser Val Asn Glu Arg Val Met Pro Ile	
	250 255 260 265
tgc cta cca tcc aag gat tat gca gaa gta ggg cgt gtg ggt tat gtt	869
Cys Leu Pro Ser Lys Asp Tyr Ala Glu Val Gly Arg Val Gly Tyr Val	
	270 275 280
tct ggc tgg ggg cga aat gcc aat ttt aaa ttt act gac cat ctg aag	917
Ser Gly Trp Gly Arg Asn Ala Asn Phe Lys Phe Thr Asp His Leu Lys	
	285 290 295
tat gtc atg ctg cct gtg gct gac caa gac caa tgc ata agg cat tat	965
Tyr Val Met Leu Pro Val Ala Asp Gln Asp Gln Cys Ile Arg His Tyr	
	300 305 310
gaa ggc agc aca gtc ccc gaa aag aag aca ccg aag agc cct gta ggg	1013
Glu Gly Ser Thr Val Pro Glu Lys Lys Thr Pro Lys Ser Pro Val Gly	
	315 320 325
gtg cag ccc ata ctg aat gaa cac acc ttc tgt gct ggc atg tct aag	1061
Val Gln Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Met Ser Lys	
	330 335 340 345
tac caa gaa gac acc tgc tat ggc gat gcg ggc agt gcc ttt gcc gtt	1109
Tyr Gln Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Val	
	350 355 360
cac gac ctg gag gag gac acc tgg tat gcg act ggg atc tta agc ttt	1157
His Asp Leu Glu Glu Asp Thr Trp Tyr Ala Thr Gly Ile Leu Ser Phe	
	365 370 375

gat	aag	agc	tgt	gct	gtg	gct	gag	tat	ggc	gtg	tat	gtg	aag	gtg	act	1205
Asp	Lys	Ser	Cys	Ala	Val	Ala	Glu	Tyr	Gly	Val	Tyr	Val	Lys	Val	Thr	
		380					385					390				

tcc	atc	cag	gac	tgg	gtt	cag	aag	acc	ata	gct	gag	aac	taa			1247
Ser	Ile	Gln	Asp	Trp	Val	Gln	Lys	Thr	Ile	Ala	Glu	Asn	*			
	395					400					405					

tgcaaggctg	gccggaagcc	cttgccctgaa	agcaagattt	cagcctggaa	gagggcaaaag	1307
tggacgggag	tggacaggag	tggatgcgat	aagatgtgg	ttgaagctga	tgggtgccag	1367
ccctgcattg	ctgagtcatt	caataaagag	ctttctttt	accca		1412

<210> 6
 <211> 406
 <212> PRT
 <213> human

<400> 6

Met	Ser	Ala	Leu	Gly	Ala	Val	Ile	Ala	Leu	Leu	Leu	Trp	Gly	Gln	Leu
1				5					10					15	
Phe	Ala	Val	Asp	Ser	Gly	Asn	Asp	Val	Thr	Asp	Ile	Ala	Asp	Asp	Gly
			20					25					30		
Cys	Pro	Lys	Pro	Pro	Glu	Ile	Ala	His	Gly	Tyr	Val	Glu	His	Ser	Val
		35					40					45			
Arg	Tyr	Gln	Cys	Lys	Asn	Tyr	Tyr	Lys	Leu	Arg	Thr	Glu	Gly	Asp	Gly
	50				55						60				
Val	Tyr	Thr	Leu	Asn	Asp	Lys	Lys	Gln	Trp	Ile	Asn	Lys	Ala	Val	Gly
	65			70					75						80
Asp	Lys	Leu	Pro	Glu	Cys	Glu	Ala	Asp	Asp	Gly	Cys	Pro	Lys	Pro	Pro
			85					90					95		
Glu	Ile	Ala	His	Gly	Tyr	Val	Glu	His	Ser	Val	Arg	Tyr	Gln	Cys	Lys
			100					105					110		
Asn	Tyr	Tyr	Lys	Leu	Arg	Thr	Glu	Gly	Asp	Gly	Val	Tyr	Thr	Leu	Asn
		115					120					125			
Asn	Glu	Lys	Gln	Trp	Ile	Asn	Lys	Ala	Val	Gly	Asp	Lys	Leu	Pro	Glu
	130				135						140				
Cys	Glu	Ala	Val	Cys	Gly	Lys	Pro	Lys	Asn	Pro	Ala	Asn	Pro	Val	Gln
	145				150				155						160
Arg	Ile	Leu	Gly	Gly	His	Leu	Asp	Ala	Lys	Gly	Ser	Phe	Pro	Trp	Gln
			165						170					175	
Ala	Lys	Met	Val	Ser	His	His	Asn	Leu	Thr	Thr	Gly	Ala	Thr	Leu	Ile
		180					185						190		
Asn	Glu	Gln	Trp	Leu	Leu	Thr	Thr	Ala	Lys	Asn	Leu	Phe	Leu	Asn	His
		195					200					205			
Ser	Glu	Asn	Ala	Thr	Ala	Lys	Asp	Ile	Ala	Pro	Thr	Leu	Thr	Leu	Tyr
	210					215					220				
Val	Gly	Lys	Lys	Gln	Leu	Val	Glu	Ile	Glu	Lys	Val	Val	Leu	His	Pro
	225			230					235						240
Asn	Tyr	Ser	Gln	Val	Asp	Ile	Gly	Leu	Ile	Lys	Leu	Lys	Gln	Lys	Val
			245					250						255	
Ser	Val	Asn	Glu	Arg	Val	Met	Pro	Ile	Cys	Leu	Pro	Ser	Lys	Asp	Tyr
		260					265						270		
Ala	Glu	Val	Gly	Arg	Val	Gly	Tyr	Val	Ser	Gly	Trp	Gly	Arg	Asn	Ala
		275					280					285			
Asn	Phe	Lys	Phe	Thr	Asp	His	Leu	Lys	Tyr	Val	Met	Leu	Pro	Val	Ala
	290					295					300				
Asp	Gln	Asp	Gln	Cys	Ile	Arg	His	Tyr	Glu	Gly	Ser	Thr	Val	Pro	Glu
	305				310					315					320
Lys	Lys	Thr	Pro	Lys	Ser	Pro	Val	Gly	Val	Gln	Pro	Ile	Leu	Asn	Glu
				325					330					335	
His	Thr	Phe	Cys	Ala	Gly	Met	Ser	Lys	Tyr	Gln	Glu	Asp	Thr	Cys	Tyr
		340						345					350		
Gly	Asp	Ala	Gly	Ser	Ala	Phe	Ala	Val	His	Asp	Leu	Glu	Glu	Asp	Thr
		355					360					365			
Trp	Tyr	Ala	Thr	Gly	Ile	Leu	Ser	Phe	Asp	Lys	Ser	Cys	Ala	Val	Ala
	370					375					380				
Glu	Tyr	Gly	Val	Tyr	Val	Lys	Val	Thr	Ser	Ile	Gln	Asp	Trp	Val	Gln
	385				390					395					400
Lys	Thr	Ile	Ala	Glu	Asn										


```
<220>
<221> CDS
<222> (88) ... (990)
```

```
<400> 7  
gcagagcaca gcatcgtcg gaccagactc gtctcaggcc agttgcagcc ttctcagcca 60  
aacgccgacc aaggaaaact cactacc atg aga att gca gtg att tgc ttt tgc 114  
Met Arg Ile Ala Val Ile Cys Phe Cys  
1 5
```

ctc cta ggc atc acc tgt gcc ata cca gtt aaa cag gct gat tct gga 162
Leu Leu Gly Ile Thr Cys Ala Ile Pro Val Lys Gln Ala Asp Ser Gly
10 15 20 25

agt tct gag gaa aag cag ctt tac aac aaa tac cca gat gct gtg gcc 210
 Ser Ser Glu Glu Lys Gln Leu Tyr Asn Lys Tyr Pro Asp Ala Val Ala
 30 35 40

aca tgg cta aac cct gac cca tct cag aag cag aat ctc cta gcc cca 258
Thr Trp Leu Asn Pro Asp Pro Ser Gln Lys Gln Asn Leu Leu Ala Pro
45 50 55

cag acc ctt cca agt aag tcc aac gaa agc cat gac cac atg gat gat 306
Gln Thr Leu Pro Ser Lys Ser Asn Glu Ser His Asp His Met Asp Asp
60 65 70

atg gat gat gaa gat gat gat gac cat gtg gac agc cag gac tcc att 354
Met Asp Asp Glu Asp Asp Asp Asp His Val Asp Ser Gln Asp Ser Ile
75 80 85

gac tcg aac gac tct gat gat gta gat gac act gat gat tct cac cag 402
Asp Ser Asn Asp Ser Asp Asp Val Asp Asp Thr Asp Asp Ser His Gln
90 95 100 105

tct	gat	gag	tct	cac	cat	tct	gat	gaa	tct	gat	gaa	ctg	gtc	act	gat	450
Ser	Asp	Glu	Ser	His	His	Ser	Asp	Glu	Ser	Asp	Glu	Leu	Val	Thr	Asp	
				110					115					120		

ttt ccc acg gac ctg cca gca acc gaa gtt ttc act cca gtt gtc ccc 498
Phe Pro Thr Asp Leu Pro Ala Thr Glu Val Phe Thr Pro Val Val Pro
125 130 135

aca gta gac aca tat gat ggc cga ggt gat agt gtg gtt tat gga ctg 546
Thr Val Asp Thr Tyr Asp Gly Arg Gly Asp Ser Val Val Tyr Gly Leu
140 145 150

agg tca aaa tct aag aag ttt cgc aga cct gac atc cag tac cct gat 594
Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile Gln Tyr Pro Asp
155 160 165

gct aca gac gag gac atc acc tca cac atg gaa agc gag gag ttg aat 642
Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser Glu Glu Leu Asn
170 175 180 185

ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg aac gcg cct tct 690
Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu Asn Ala Pro Ser
190 195 200

gat tgg gac agc cgt ggg aag gac agt tat gaa acg agt cag ctg gat 738
Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr Ser Gln Leu Asp
205 210 215

```

gac cag agt gct gaa acc cac agc cac aag cag tcc aga tta tat aag 786
Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser Arg Leu Tyr Lys
220 225 230

cgg aaa gcc aat gat gag agc aat gag cat tcc gat gtg att gat agt 834
Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp Val Ile Asp Ser
235 240 245

cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc cat gaa ttt cac 882
Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser His Glu Phe His
250 255 260 265

agc cat gaa gat atg ctg gtt gta gac ccc aaa agt aag gaa gaa gat 930
Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser Lys Glu Glu Asp
270 275 280

aaa cac ctg aaa ttt cgt att tct cat gaa tta gat agt gca tct tct 978
Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp Ser Ala Ser Ser
285 290 295

gag gtc aat taa aaggagaaaa aatacaattt ctcactttgc atttagtcaa 1030
Glu Val Asn *
300

aagaaaaaat gctttatagc aaaatgaaag agaacatgaa atgctttcttt ctcagttttat 1090
tggttgaatg tgtatctatt tgagtcctgga aataactaat gtgtttgata attagttttag 1150
tttgtggctt catggaaact ccctgtaaac taaaagcttc aggggttatgt ctatgttcat 1210
tctatagaag aaatgcaaac tatcactgta ttttaatat tgttattctc tcatgaatag 1270
aaattttatgt agaagcaaac aaaatacttt taccacttta aaaagagaat ataacatttt 1330
atgtcactat aatcttttgt tttttaagtt agtgtatat ttgttgtgat tatctttttg 1390
tggtgtgaat aaatctttta tcttgaatgt aataagaatt tggtggtgtc aattgcttat 1450
ttgttttccc acggttggtcc agcaattaat aaaacataac ctttttttact gcctaaaaaa 1510
aaaaaaaaaa aaaa 1524

<210> 8
<211> 300
<212> PRT
<213> human

<400> 8
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1 5 10 15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20 25 30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
35 40 45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
50 55 60
Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
65 70 75 80
Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp
85 90 95
Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
100 105 110
Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
115 120 125
Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
130 135 140
Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
145 150 155 160
Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
165 170 175
Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
180 185 190
Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
195 200 205
Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His
210 215 220

```

Ser	His	Lys	Gln	Ser	Arg	Leu	Tyr	Lys	Arg	Lys	Ala	Asn	Asp	Glu	Ser
225					230					235					240
Asn	Glu	His	Ser	Asp	Val	Ile	Asp	Ser	Gln	Glu	Leu	Ser	Lys	Val	Ser
				245					250					255	
Arg	Glu	Phe	His	Ser	His	Glu	Phe	His	Ser	His	Glu	Asp	Met	Leu	Val
			260					265					270		
Val	Asp	Pro	Lys	Ser	Lys	Glu	Glu	Asp	Lys	His	Leu	Lys	Phe	Arg	Ile
		275					280					285			
Ser	His	Glu	Leu	Asp	Ser	Ala	Ser	Ser	Glu	Val	Asn				
	290					295					300				

<210> 9
 <211> 2657
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (589)...(2022)

<400> 9
 aggggagagtc tgcccacaag tttttgtata ttttctcact gaggcacata ttcagtttgg 60
 gcagcagaca ctgagcagaa cgtagcacgg caatgcttgg tagcaatgcc tgtccggcca 120
 gcactcagaa gacggaggca ggagaatcat agcttccagt cagcctcttc tacaatatag 180
 tcagttggaa gtcagccagc ttagacaaca tggagagcct gtgccgaaag ccactgggta 240
 agcccgaatc tcagtagcag agagctgccc aggggtgcgta ctgcaaaaaa aaaacctcaa 300
 acaacagaag tagggagggtg taaaataaag tgtagggggg tgggaatttaa gctgatgtgg 360
 acttccaaat aaagttacct tttagatacc tatttaaatac aatagcatag acctgaaact 420
 gtctatcaga aaatgtgtct attctgagga aggagtgcata acgaggttct gtgagggggg 480
 cctctggctt tgagagggtg taccatcaca taagactcct aaaagcacat acttttataa 540
 attcaccatg agctttaaca tcttctttgt catttcgcag actgagcc atg gag tct 597
 Met Glu Ser
 1

ttc gat gct gac acc aat tca act gac cta cac tca cgg cct ctg ttt 645
 Phe Asp Ala Asp Thr Asn Ser Thr Asp Leu His Ser Arg Pro Leu Phe
 5 10 15

caa ccc caa gac att gcc tcc atg gtc att ctt ggt ctc act tgt cta 693
 Gln Pro Gln Asp Ile Ala Ser Met Val Ile Leu Gly Leu Thr Cys Leu
 20 25 30 35

ttg gga ctg cta ggc aat ggg ctg gtg ctg tgg gta gct ggc gta aag 741
 Leu Gly Leu Leu Gly Asn Gly Leu Val Leu Trp Val Ala Gly Val Lys
 40 45 50

atg aag acg acc gtg aac aca gtc tgg ttc ctc cat ctc acc ctg gcc 789
 Met Lys Thr Thr Val Asn Thr Val Trp Phe Leu His Leu Thr Leu Ala
 55 60 65

gat ttc ctc tgc tgc ctc tcc ttg ccc ttc tcc ttg gct cac ctg att 837
 Asp Phe Leu Cys Cys Leu Ser Leu Pro Phe Ser Leu Ala His Leu Ile
 70 75 80

ctc caa gga cac tgg ccc tat ggc ttg ttc ctg tgc aaa ctt atc cca 885
 Leu Gln Gly His Trp Pro Tyr Gly Leu Phe Leu Cys Lys Leu Ile Pro
 85 90 95

tcc atc att att ctc aac atg ttt gcc agt gtc ttc ctg ctt act gcc 933
 Ser Ile Ile Ile Leu Asn Met Phe Ala Ser Val Phe Leu Leu Thr Ala
 100 105 110 115

att agc ctg gac cga tgt ctg ata gta cat aag cca atc tgg tgc cag 981
 Ile Ser Leu Asp Arg Cys Leu Ile Val His Lys Pro Ile Trp Cys Gln
 120 125 130

aat cat cga aac gtg aga acc gcc ttc gcc atc tgt gga tgt gtc tgg 1029
 Asn His Arg Asn Val Arg Thr Ala Phe Ala Ile Cys Gly Cys Val Trp

135				140				145								
gtg	gta	gcc	ttt	gtg	atg	tgt	gtg	ccc	gta	ttt	gta	tac	cgt	gat	ctg	1077
Val	Val	Ala	Phe	Val	Met	Cys	Val	Pro	Val	Phe	Val	Tyr	Arg	Asp	Leu	
		150					155					160				
ttc	att	atg	gac	aat	cgc	agt	ata	tgt	aga	tat	aat	ttt	gat	tcc	tcc	1125
Phe	Ile	Met	Asp	Asn	Arg	Ser	Ile	Cys	Arg	Tyr	Asn	Phe	Asp	Ser	Ser	
	165					170					175					
agg	tca	tat	gat	tat	tgg	gac	tac	gtg	tac	aaa	cta	agt	cta	cca	gaa	1173
Arg	Ser	Tyr	Asp	Tyr	Trp	Asp	Tyr	Val	Tyr	Lys	Leu	Ser	Leu	Pro	Glu	
180					185					190					195	
agc	aat	tct	act	gat	aac	tcc	act	gct	cag	cta	act	gga	cat	atg	aat	1221
Ser	Asn	Ser	Thr	Asp	Asn	Ser	Thr	Ala	Gln	Leu	Thr	Gly	His	Met	Asn	
				200					205					210		
gac	agg	tca	gct	cct	tcc	tct	gta	cag	gca	agg	gat	tac	ttt	tgg	aca	1269
Asp	Arg	Ser	Ala	Pro	Ser	Ser	Val	Gln	Ala	Arg	Asp	Tyr	Phe	Trp	Thr	
			215					220					225			
gtt	acc	act	gcc	ctc	cag	tca	cag	cca	ttc	cta	aca	tct	cct	gaa	gac	1317
Val	Thr	Thr	Ala	Leu	Gln	Ser	Gln	Pro	Phe	Leu	Thr	Ser	Pro	Glu	Asp	
		230					235					240				
tca	ttc	tct	cta	gat	tca	gca	aac	caa	caa	ccc	cat	tat	ggg	gga	aag	1365
Ser	Phe	Ser	Leu	Asp	Ser	Ala	Asn	Gln	Gln	Pro	His	Tyr	Gly	Gly	Lys	
	245					250					255					
cct	cct	aat	gtc	ctc	aca	gcc	gcc	gta	ccc	agc	ggg	ttt	cct	gtt	gaa	1413
Pro	Pro	Asn	Val	Leu	Thr	Ala	Ala	Val	Pro	Ser	Gly	Phe	Pro	Val	Glu	
260					265					270					275	
gat	cgt	aaa	tcc	aat	aca	ctg	aac	gct	gac	gct	ttt	ctc	tct	gct	cac	1461
Asp	Arg	Lys	Ser	Asn	Thr	Leu	Asn	Ala	Asp	Ala	Phe	Leu	Ser	Ala	His	
				280					285					290		
aca	gaa	ctt	ttc	cct	act	gct	tct	agt	ggg	cat	tta	tac	ccc	tat	gat	1509
Thr	Glu	Leu	Phe	Pro	Thr	Ala	Ser	Ser	Gly	His	Leu	Tyr	Pro	Tyr	Asp	
		295						300					305			
ttc	cag	ggg	gat	tat	gtt	gac	caa	ttc	acg	tat	gac	aat	cat	gtg	ccg	1557
Phe	Gln	Gly	Asp	Tyr	Val	Asp	Gln	Phe	Thr	Tyr	Asp	Asn	His	Val	Pro	
		310					315					320				
aca	ccg	ctg	atg	gca	ata	acc	atc	aca	agg	ctg	gtg	gtg	ggc	ttc	ctg	1605
Thr	Pro	Leu	Met	Ala	Ile	Thr	Ile	Thr	Arg	Leu	Val	Val	Gly	Phe	Leu	
	325					330					335					
gtg	ccg	ttt	ttc	atc	atg	gta	att	tgt	tac	agc	ctc	atc	gtc	ttc	aga	1653
Val	Pro	Phe	Phe	Ile	Met	Val	Ile	Cys	Tyr	Ser	Leu	Ile	Val	Phe	Arg	
340					345					350					355	
atg	cga	aaa	acc	aac	ttc	acc	aag	tct	cgg	aac	aaa	acc	ttt	cgg	gtg	1701
Met	Arg	Lys	Thr	Asn	Phe	Thr	Lys	Ser	Arg	Asn	Lys	Thr	Phe	Arg	Val	
				360					365					370		
gct	gtg	gct	gtg	gtc	act	gtc	ttt	ttt	atc	tgc	tgg	act	cca	tac	cat	1749
Ala	Val	Ala	Val	Val	Thr	Val	Phe	Phe	Ile	Cys	Trp	Thr	Pro	Tyr	His	
			375					380					385			
ctt	gtc	gga	gtc	ctg	cta	ttg	att	act	gat	cca	gaa	agt	tcc	ttg	ggg	1797
Leu	Val	Gly	Val	Leu	Leu	Leu	Ile	Thr	Asp	Pro	Glu	Ser	Ser	Leu	Gly	
		390					395					400				
gaa	gct	gtg	atg	tcc	tgg	gac	cac	atg	tcc	att	gct	tta	gca	tct	gcc	1845
Glu	Ala	Val	Met	Ser	Trp	Asp	His	Met	Ser	Ile	Ala	Leu	Ala	Ser	Ala	
	405					410					415					

aat agt tgc ttc aac cct ttc ctg tat gcc ctc ttg ggg aaa gac ttt 1893
 Asn Ser Cys Phe Asn Pro Phe Leu Tyr Ala Leu Gly Lys Asp Phe
 420 425 430 435

agg aag aaa gca aga cag tct ata aag ggc att ctg gaa gca gcc ttc 1941
 Arg Lys Lys Ala Arg Gln Ser Ile Lys Gly Ile Leu Glu Ala Ala Phe
 440 445 450

agc gaa gag ctc acg cac tct acc aac tgt acc caa gac aaa gcc tct 1989
 Ser Glu Glu Leu Thr His Ser Thr Asn Cys Thr Gln Asp Lys Ala Ser
 455 460 465

tca aaa aga aac aat atg agt aca gat gtg tga agatgtggcc ctgggaacct 2042
 Ser Lys Arg Asn Asn Met Ser Thr Asp Val *
 470 475

aagcagagtt ctcaggtgaa cagtgatgga tgacatgtga gcaggacact ttagacaatt 2102
 tggcgactct cagagaaagg tctcttattg acatcagcat catttgaaaa cattaaagat 2162
 gcaaaatttc aagcccatc ccagatgtgt tgactcagaa tctctggccc atgggaccag 2222
 tgttttaaca ggccttcttg tttccatcag tgtaaagttt tacctcattt ggcttagtct 2282
 attcccatcc ctgactacac catgtgcaat gaataacttt ttcattctgtt ttcagtattc 2342
 tttttttttc cttagcatca tctaaacttc tagtttgcat ggaaggctgc tcttattgtt 2402
 ctgaatggaa gatattcatt tattgtacag ttttgtggtg gtgacaagtg atttttaagt 2462
 ggggaaagag acacagtaag aaaagatcta tgaaagcagg gagtgttgag ttagagtttg 2522
 acagaacaca gtgccaaatg ccaccacta aaagcaacct gagataattc cagtgttcatt 2582
 gtgagcaagt gagcacagat acacataaac actttcctac tcctggagtg ttttagaagt 2642
 tgtagcttgg agctc 2657

<210> 10
 <211> 477
 <212> PRT
 <213> mouse

<400> 10
 Met Glu Ser Phe Asp Ala Asp Thr Asn Ser Thr Asp Leu His Ser Arg
 1 5 10 15
 Pro Leu Phe Gln Pro Gln Asp Ile Ala Ser Met Val Ile Leu Gly Leu
 20 25 30
 Thr Cys Leu Leu Gly Leu Leu Gly Asn Gly Leu Val Leu Trp Val Ala
 35 40 45
 Gly Val Lys Met Lys Thr Thr Val Asn Thr Val Trp Phe Leu His Leu
 50 55 60
 Thr Leu Ala Asp Phe Leu Cys Cys Leu Ser Leu Pro Phe Ser Leu Ala
 65 70 75 80
 His Leu Ile Leu Gln Gly His Trp Pro Tyr Gly Leu Phe Leu Cys Lys
 85 90 95
 Leu Ile Pro Ser Ile Ile Ile Leu Asn Met Phe Ala Ser Val Phe Leu
 100 105 110
 Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Ile Val His Lys Pro Ile
 115 120 125
 Trp Cys Gln Asn His Arg Asn Val Arg Thr Ala Phe Ala Ile Cys Gly
 130 135 140
 Cys Val Trp Val Val Ala Phe Val Met Cys Val Pro Val Phe Val Tyr
 145 150 155 160
 Arg Asp Leu Phe Ile Met Asp Asn Arg Ser Ile Cys Arg Tyr Asn Phe
 165 170 175
 Asp Ser Ser Arg Ser Tyr Asp Tyr Trp Asp Tyr Val Tyr Lys Leu Ser
 180 185 190
 Leu Pro Glu Ser Asn Ser Thr Asp Asn Ser Thr Ala Gln Leu Thr Gly
 195 200 205
 His Met Asn Asp Arg Ser Ala Pro Ser Ser Val Gln Ala Arg Asp Tyr
 210 215 220
 Phe Trp Thr Val Thr Thr Ala Leu Gln Ser Gln Pro Phe Leu Thr Ser
 225 230 235 240
 Pro Glu Asp Ser Phe Ser Leu Asp Ser Ala Asn Gln Gln Pro His Tyr
 245 250 255
 Gly Gly Lys Pro Asn Val Leu Thr Ala Ala Val Pro Ser Gly Phe
 260 265 270

Pro	Val	Glu	Asp	Arg	Lys	Ser	Asn	Thr	Leu	Asn	Ala	Asp	Ala	Phe	Leu
		275					280					285			
Ser	Ala	His	Thr	Glu	Leu	Phe	Pro	Thr	Ala	Ser	Ser	Gly	His	Leu	Tyr
	290					295					300				
Pro	Tyr	Asp	Phe	Gln	Gly	Asp	Tyr	Val	Asp	Gln	Phe	Thr	Tyr	Asp	Asn
305					310					315					320
His	Val	Pro	Thr	Pro	Leu	Met	Ala	Ile	Thr	Ile	Thr	Arg	Leu	Val	Val
				325					330					335	
Gly	Phe	Leu	Val	Pro	Phe	Phe	Ile	Met	Val	Ile	Cys	Tyr	Ser	Leu	Ile
			340					345					350		
Val	Phe	Arg	Met	Arg	Lys	Thr	Asn	Phe	Thr	Lys	Ser	Arg	Asn	Lys	Thr
		355					360					365			
Phe	Arg	Val	Ala	Val	Ala	Val	Val	Thr	Val	Phe	Phe	Ile	Cys	Trp	Thr
	370					375					380				
Pro	Tyr	His	Leu	Val	Gly	Val	Leu	Leu	Leu	Ile	Thr	Asp	Pro	Glu	Ser
385					390					395					400
Ser	Leu	Gly	Glu	Ala	Val	Met	Ser	Trp	Asp	His	Met	Ser	Ile	Ala	Leu
				405					410					415	
Ala	Ser	Ala	Asn	Ser	Cys	Phe	Asn	Pro	Phe	Leu	Tyr	Ala	Leu	Leu	Gly
			420				425						430		
Lys	Asp	Phe	Arg	Lys	Lys	Ala	Arg	Gln	Ser	Ile	Lys	Gly	Ile	Leu	Glu
		435					440					445			
Ala	Ala	Phe	Ser	Glu	Glu	Leu	Thr	His	Ser	Thr	Asn	Cys	Thr	Gln	Asp
	450					455					460				
Lys	Ala	Ser	Ser	Lys	Arg	Asn	Asn	Met	Ser	Thr	Asp	Val			
465					470					475					

<210> 11
 <211> 1109
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (84)...(1085)

<400> 11
 actcacacaa tctacctggt tgattttgctt aggaccccat agataacagc agcttttga 60
 tcaactatga tcactatgga acc atg gat cct aac ata cct gcg gat ggc att 113
 Met Asp Pro Asn Ile Pro Ala Asp Gly Ile
 1 5 10

cac ctc ccg aag cgg caa cct ggg gat gtt gca gcc ctt atc atc tac 161
 His Leu Pro Lys Arg Gln Pro Gly Asp Val Ala Ala Leu Ile Ile Tyr 25
 15 20 25

tcg gtg gtg ttc ctg gtg gga gta ccc ggg aat gcc ctg gtg gtg tgg 209
 Ser Val Val Phe Leu Val Gly Val Pro Gly Asn Ala Leu Val Val Trp 40
 30 35 40

gtg aca gcc ttc gag cca gac ggg ccg tca aac gcc atc tgg ttt ctg 257
 Val Thr Ala Phe Glu Pro Asp Gly Pro Ser Asn Ala Ile Trp Phe Leu 55
 45 50 55

aat ctg gcg gtg gcc gac ctc ctc tcg tgc ttg gcc atg cct gtc ctg 305
 Asn Leu Ala Val Ala Asp Leu Leu Ser Cys Leu Ala Met Pro Val Leu 60
 60 65 70

ttc acg acc gtt tta aat cat aac tac tgg tac ttt gat gcc acc gcc 353
 Phe Thr Thr Val Leu Asn His Asn Tyr Trp Tyr Phe Asp Ala Thr Ala 80
 75 80 85 90

tgt ata gtc ctg ccc tcg ctc atc ctg ctc aac atg tac gcc agt atc 401
 Cys Ile Val Leu Pro Ser Leu Ile Leu Leu Asn Met Tyr Ala Ser Ile 95
 95 100 105

ctg ctg ctg gct acc att agt gcc gac cgt ttc ctg ctg gtg ttc aag 449
 Leu Leu Leu Ala Thr Ile Ser Ala Asp Arg Phe Leu Leu Val Phe Lys

110					115					120						
ccc	atc	tgg	tgt	cag	aag	gtc	cgc	ggg	act	ggc	ctg	gca	tgg	atg	gcc	497
Pro	Ile	Trp	Cys	Gln	Lys	Val	Arg	Gly	Thr	Gly	Leu	Ala	Trp	Met	Ala	
		125					130					135				
tgt	gga	gtg	gcc	tgg	gtc	tta	gca	ttg	ctc	ctc	acc	att	cca	tcc	ttc	545
Cys	Gly	Val	Ala	Trp	Val	Leu	Ala	Leu	Leu	Leu	Thr	Ile	Pro	Ser	Phe	
	140					145					150					
gtg	tac	cgg	gag	gca	tat	aag	gac	ttc	tac	tca	gag	cac	act	gta	tgt	593
Val	Tyr	Arg	Glu	Ala	Tyr	Lys	Asp	Phe	Tyr	Ser	Glu	His	Thr	Val	Cys	
155					160					165					170	
ggg	att	aac	tat	ggg	ggg	ggg	agc	ttc	ccc	aaa	gag	aag	gct	gtg	gcc	641
Gly	Ile	Asn	Tyr	Gly	Gly	Gly	Ser	Phe	Pro	Lys	Glu	Lys	Ala	Val	Ala	
				175					180					185		
atc	ctg	cgg	ctg	atg	gtg	ggg	ttt	gtg	ttg	cct	ctg	ctc	act	cta	aac	689
Ile	Leu	Arg	Leu	Met	Val	Gly	Phe	Val	Leu	Pro	Leu	Leu	Thr	Leu	Asn	
			190					195					200			
atc	tgc	tac	acc	ttc	ctc	ctg	ctc	cgg	acc	tgg	agt	cgc	aag	gcc	acg	737
Ile	Cys	Tyr	Thr	Phe	Leu	Leu	Leu	Arg	Thr	Trp	Ser	Arg	Lys	Ala	Thr	
		205					210					215				
cgc	tcc	acc	aag	acg	ctc	aaa	gtg	gtg	atg	gct	gtg	gtc	atc	tgt	ttc	785
Arg	Ser	Thr	Lys	Thr	Leu	Lys	Val	Val	Met	Ala	Val	Val	Ile	Cys	Phe	
	220					225					230					
ttt	atc	ttc	tgg	ctg	ccc	tat	cag	gtg	acc	ggg	gtg	atg	ata	gcg	tgg	833
Phe	Ile	Phe	Trp	Leu	Pro	Tyr	Gln	Val	Thr	Gly	Val	Met	Ile	Ala	Trp	
235					240					245					250	
ctg	ccc	ccg	tcc	tcg	ccc	acc	ttg	aag	agg	gtg	gag	aag	ctg	aac	tcc	881
Leu	Pro	Pro	Ser	Ser	Pro	Thr	Leu	Lys	Arg	Val	Glu	Lys	Leu	Asn	Ser	
				255					260					265		
ctg	tgc	gtg	tcc	ctg	gcc	tac	atc	aac	tgc	tgt	gtt	aac	cct	atc	atc	929
Leu	Cys	Val	Ser	Leu	Ala	Tyr	Ile	Asn	Cys	Cys	Val	Asn	Pro	Ile	Ile	
			270					275					280			
tac	gtc	atg	gct	ggc	cag	ggg	ttc	cat	gga	cga	ctc	cta	agg	tct	ctc	977
Tyr	Val	Met	Ala	Gly	Gln	Gly	Phe	His	Gly	Arg	Leu	Leu	Arg	Ser	Leu	
		285					290					295				
ccc	agc	atc	ata	cga	aac	gct	ctc	tct	gag	gat	tca	gtg	ggc	agg	gat	1025
Pro	Ser	Ile	Ile	Arg	Asn	Ala	Leu	Ser	Glu	Asp	Ser	Val	Gly	Arg	Asp	
	300					305					310					
agc	aag	act	ttc	act	ccg	tcc	aca	gac	gac	acc	tca	acc	cgg	aag	agt	1073
Ser	Lys	Thr	Phe	Thr	Pro	Ser	Thr	Asp	Asp	Thr	Ser	Thr	Arg	Lys	Ser	
315					320					325					330	
cag	gcg	gtg	tag	aggagaagcc	acaactggcc	tagc										1109
Gln	Ala	Val	*													

<210> 12
 <211> 333
 <212> PRT
 <213> mouse

<400> 12
 Met Asp Pro Asn Ile Pro Ala Asp Gly Ile His Leu Pro Lys Arg Gln
 1 5 10 15
 Pro Gly Asp Val Ala Ala Leu Ile Ile Tyr Ser Val Val Phe Leu Val
 20 25 30

Gly	Val	Pro	Gly	Asn	Ala	Leu	Val	Val	Trp	Val	Thr	Ala	Phe	Glu	Pro
		35					40					45			
Asp	Gly	Pro	Ser	Asn	Ala	Ile	Trp	Phe	Leu	Asn	Leu	Ala	Val	Ala	Asp
	50					55					60				
Leu	Leu	Ser	Cys	Leu	Ala	Met	Pro	Val	Leu	Phe	Thr	Thr	Val	Leu	Asn
65					70					75					80
His	Asn	Tyr	Trp	Tyr	Phe	Asp	Ala	Thr	Ala	Cys	Ile	Val	Leu	Pro	Ser
				85					90					95	
Leu	Ile	Leu	Leu	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu	Leu	Ala	Thr	Ile
			100					105					110		
Ser	Ala	Asp	Arg	Phe	Leu	Leu	Val	Phe	Lys	Pro	Ile	Trp	Cys	Gln	Lys
		115					120					125			
Val	Arg	Gly	Thr	Gly	Leu	Ala	Trp	Met	Ala	Cys	Gly	Val	Ala	Trp	Val
	130					135					140				
Leu	Ala	Leu	Leu	Leu	Thr	Ile	Pro	Ser	Phe	Val	Tyr	Arg	Glu	Ala	Tyr
145					150					155					160
Lys	Asp	Phe	Tyr	Ser	Glu	His	Thr	Val	Cys	Gly	Ile	Asn	Tyr	Gly	Gly
				165					170					175	
Gly	Ser	Phe	Pro	Lys	Glu	Lys	Ala	Val	Ala	Ile	Leu	Arg	Leu	Met	Val
			180					185					190		
Gly	Phe	Val	Leu	Pro	Leu	Leu	Thr	Leu	Asn	Ile	Cys	Tyr	Thr	Phe	Leu
		195					200					205			
Leu	Leu	Arg	Thr	Trp	Ser	Arg	Lys	Ala	Thr	Arg	Ser	Thr	Lys	Thr	Leu
	210					215					220				
Lys	Val	Val	Met	Ala	Val	Val	Ile	Cys	Phe	Phe	Ile	Phe	Trp	Leu	Pro
225					230					235					240
Tyr	Gln	Val	Thr	Gly	Val	Met	Ile	Ala	Trp	Leu	Pro	Pro	Ser	Ser	Pro
				245					250					255	
Thr	Leu	Lys	Arg	Val	Glu	Lys	Leu	Asn	Ser	Leu	Cys	Val	Ser	Leu	Ala
			260					265					270		
Tyr	Ile	Asn	Cys	Cys	Val	Asn	Pro	Ile	Ile	Tyr	Val	Met	Ala	Gly	Gln
		275					280					285			
Gly	Phe	His	Gly	Arg	Leu	Leu	Arg	Ser	Leu	Pro	Ser	Ile	Ile	Arg	Asn
	290					295					300				
Ala	Leu	Ser	Glu	Asp	Ser	Val	Gly	Arg	Asp	Ser	Lys	Thr	Phe	Thr	Pro
305					310					315					320
Ser	Thr	Asp	Asp	Thr	Ser	Thr	Arg	Lys	Ser	Gln	Ala	Val			
				325					330						

<210> 13
 <211> 1267
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (49)...(1092)

<400> 13
 gaattcggca cgagcagccc ttccagagag aggcaagaga ggtccacg atg aga gcc 57
 Met Arg Ala
 1

ctg gga gct gtt gtc act ctc ctg ctc tgg ggt cag ctt ttt gct gtg 105
 Leu Gly Ala Val Val Thr Leu Leu Leu Trp Gly Gln Leu Phe Ala Val
 5 10 15

gag ttg ggc aat gat gcc atg gac ttt gaa gat gac agc tgc cca aag 153
 Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Asp Ser Cys Pro Lys
 20 25 30 35

ccc cca gag att gca aac ggc tat gtg gag cac ttg gtt cgc tat cgc 201
 Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val Arg Tyr Arg
 40 45 50

tgc cga cag ttc tac aga cta cgg gcc gaa gga gat ggg gtg tac acc 249
 Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly Val Tyr Thr
 55 60 65

tta	aac	gac	gag	aag	caa	tgg	gtg	aac	aca	gtc	gct	gga	gag	aaa	ctc	297
Leu	Asn	Asp	Glu	Lys	Gln	Trp	Val	Asn	Thr	Val	Ala	Gly	Glu	Lys	Leu	
		70					75					80				
ccc	gaa	tgt	gag	gca	gtg	tgt	ggg	aag	ccc	aag	cac	cct	gtg	gac	cag	345
Pro	Glu	Cys	Glu	Ala	Val	Cys	Gly	Lys	Pro	Lys	His	Pro	Val	Asp	Gln	
	85					90					95					
gtg	cag	cgc	atc	atc	ggg	ggc	tct	atg	gat	gcc	aaa	ggc	agc	ttt	cct	393
Val	Gln	Arg	Ile	Ile	Gly	Gly	Ser	Met	Asp	Ala	Lys	Gly	Ser	Phe	Pro	
100					105					110					115	
tgg	cag	gcc	aag	atg	atc	tcc	cgc	cac	gga	ctc	acc	acc	ggg	gcc	acg	441
Trp	Gln	Ala	Lys	Met	Ile	Ser	Arg	His	Gly	Leu	Thr	Thr	Gly	Ala	Thr	
				120					125					130		
ttg	atc	agt	gac	cag	tgg	ctg	ctg	acc	acg	gcc	aaa	aac	ctc	ttc	ctg	489
Leu	Ile	Ser	Asp	Gln	Trp	Leu	Leu	Thr	Thr	Ala	Lys	Asn	Leu	Phe	Leu	
			135					140					145			
aac	cac	agc	gag	acg	gcg	tca	gcc	aag	gac	atc	acc	ccc	acc	cta	acg	537
Asn	His	Ser	Glu	Thr	Ala	Ser	Ala	Lys	Asp	Ile	Thr	Pro	Thr	Leu	Thr	
		150					155					160				
ctc	tac	gtg	ggg	aaa	aac	cag	ctg	gtg	gag	att	gag	aag	gtc	gtt	ctc	585
Leu	Tyr	Val	Gly	Lys	Asn	Gln	Leu	Val	Glu	Ile	Glu	Lys	Val	Val	Leu	
	165					170					175					
cac	ccc	aac	cac	tcc	gtg	gtg	gat	atc	ggg	cta	atc	aaa	ctc	aag	cag	633
His	Pro	Asn	His	Ser	Val	Val	Asp	Ile	Gly	Leu	Ile	Lys	Leu	Lys	Gln	
180					185					190					195	
agg	gtg	ctt	gta	acc	gag	aga	gtc	atg	cct	atc	tgc	ctg	cct	tcc	aaa	681
Arg	Val	Leu	Val	Thr	Glu	Arg	Val	Met	Pro	Ile	Cys	Leu	Pro	Ser	Lys	
				200					205					210		
gac	tac	ata	gca	cca	ggc	cgt	gtg	ggc	tac	gtg	tct	ggc	tgg	ggg	cgg	729
Asp	Tyr	Ile	Ala	Pro	Gly	Arg	Val	Gly	Tyr	Val	Ser	Gly	Trp	Gly	Arg	
			215					220					225			
aac	gcc	aac	ttt	aga	ttt	acc	gat	cgt	ctc	aag	tat	gtc	atg	ctg	cct	777
Asn	Ala	Asn	Phe	Arg	Phe	Thr	Asp	Arg	Leu	Lys	Tyr	Val	Met	Leu	Pro	
		230					235					240				
gtg	gcc	gac	cag	gac	aag	tgt	gtg	gtg	cac	tat	gag	aat	agt	aca	gtg	825
Val	Ala	Asp	Gln	Asp	Lys	Cys	Val	Val	His	Tyr	Glu	Asn	Ser	Thr	Val	
	245					250					255					
ccc	gag	aag	aaa	aac	ttg	acg	agt	ccc	gtt	ggg	gtc	cag	cct	atc	ttg	873
Pro	Glu	Lys	Lys	Asn	Leu	Thr	Ser	Pro	Val	Gly	Val	Gln	Pro	Ile	Leu	
260					265					270					275	
aac	gag	cac	acc	ttc	tgt	gct	ggc	ctc	acc	aag	tac	cag	gaa	gac	acc	921
Asn	Glu	His	Thr	Phe	Cys	Ala	Gly	Leu	Thr	Lys	Tyr	Gln	Glu	Asp	Thr	
				280					285					290		
tgc	tac	ggg	gac	gcc	ggc	agt	gcc	ttt	gcc	att	cat	gac	atg	gag	gag	969
Cys	Tyr	Gly	Asp	Ala	Gly	Ser	Ala	Phe	Ala	Ile	His	Asp	Met	Glu	Glu	
			295					300					305			
gac	acc	tgg	tac	gca	gct	ggg	atc	ctg	agc	ttt	gac	aag	agc	tgc	gct	1017
Asp	Thr	Trp	Tyr	Ala	Ala	Gly	Ile	Leu	Ser	Phe	Asp	Lys	Ser	Cys	Ala	
		310					315					320				
gtc	gct	gag	tat	ggg	gtg	tac	gtg	agg	gcg	acc	gac	ctg	aag	gac	tgg	1065
Val	Ala	Glu	Tyr	Gly	Val	Tyr	Val	Arg	Ala	Thr	Asp	Leu	Lys	Asp	Trp	
	325					330					335					

gtt cag gaa acc atg gcc aag aac tag ttcagggctc actagaaggc 1112
 Val Gln Glu Thr Met Ala Lys Asn *
 340 345

tgacatggc agggcaggct gggagccatg gaagaggggg aagtgggaagg gttgggctat 1172
 actctgatgg gttctagccc tgcactgctc agtcaacaat aaaaaaatgt gctttggacc 1232
 cataaaaaaa aaaaaaaaaa aaaaaaaggg aattc 1267

<210> 14
 <211> 347
 <212> PRT
 <213> mouse

<400> 14
 Met Arg Ala Leu Gly Ala Val Val Thr Leu Leu Leu Trp Gly Gln Leu
 1 5 10 15
 Phe Ala Val Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Ser
 20 25 30
 Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val
 35 40 45
 Arg Tyr Arg Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly
 50 55 60
 Val Tyr Thr Leu Asn Asp Glu Lys Gln Trp Val Asn Thr Val Ala Gly
 65 70 75 80
 Glu Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys His Pro
 85 90 95
 Val Asp Gln Val Gln Arg Ile Ile Gly Gly Ser Met Asp Ala Lys Gly
 100 105 110
 Ser Phe Pro Trp Gln Ala Lys Met Ile Ser Arg His Gly Leu Thr Thr
 115 120 125
 Gly Ala Thr Leu Ile Ser Asp Gln Trp Leu Leu Thr Thr Ala Lys Asn
 130 135 140
 Leu Phe Leu Asn His Ser Glu Thr Ala Ser Ala Lys Asp Ile Thr Pro
 145 150 155 160
 Thr Leu Thr Leu Tyr Val Gly Lys Asn Gln Leu Val Glu Ile Glu Lys
 165 170 175
 Val Val Leu His Pro Asn His Ser Val Val Asp Ile Gly Leu Ile Lys
 180 185 190
 Leu Lys Gln Arg Val Leu Val Thr Glu Arg Val Met Pro Ile Cys Leu
 195 200 205
 Pro Ser Lys Asp Tyr Ile Ala Pro Gly Arg Val Gly Tyr Val Ser Gly
 210 215 220
 Trp Gly Arg Asn Ala Asn Phe Arg Phe Thr Asp Arg Leu Lys Tyr Val
 225 230 235 240
 Met Leu Pro Val Ala Asp Gln Asp Lys Cys Val Val His Tyr Glu Asn
 245 250 255
 Ser Thr Val Pro Glu Lys Lys Asn Leu Thr Ser Pro Val Gly Val Gln
 260 265 270
 Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Leu Thr Lys Tyr Gln
 275 280 285
 Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Ile His Asp
 290 295 300
 Met Glu Glu Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp Lys
 305 310 315 320
 Ser Cys Ala Val Ala Glu Tyr Gly Val Tyr Val Arg Ala Thr Asp Leu
 325 330 335
 Lys Asp Trp Val Gln Glu Thr Met Ala Lys Asn
 340 345

<210> 15
 <211> 1385
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (70) ... (954)

<400> 15
cttgcttggg ttgtcagtct tctgcggcag gcattctcgg aggaaaccag ccaaggacta 60
actacgacc atg aga ttg gca gtg att tgc ttt tgc ctg ttt ggc att gcc 111
Met Arg Leu Ala Val Ile Cys Phe Cys Leu Phe Gly Ile Ala
1 5 10

tcc tcc ctc ccg gtg aaa gtg act gat tct ggc agc tca gag gag aag 159
Ser Ser Leu Pro Val Lys Val Thr Asp Ser Gly Ser Ser Glu Glu Lys 30
15 20 25 30

ctt tac agc ctg cac cca gat cct ata gcc aca tgg ctg gtg cct gac 207
Leu Tyr Ser Leu His Pro Asp Pro Ile Ala Thr Trp Leu Val Pro Asp 45
35 40 45

cca tct cag aag cag aat ctc ctt gcg cca cag aat gct gtg tcc tct 255
Pro Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser 60
50 55 60

gaa gaa aag gat gac ttt aag caa gaa act ctt cca agc aat tcc aat 303
Glu Glu Lys Asp Asp Phe Lys Gln Glu Thr Leu Pro Ser Asn Ser Asn 75
65 70 75

gaa agc cat gac cac atg gac gac gat gat gac gat gat gac gat 351
Glu Ser His Asp His Met Asp Asp Asp Asp Asp Asp Asp Asp Asp 90
80 85 90

gga gac cat gca ggg agc gag gat tct gtg gac tcg gat gaa tct gac 399
Gly Asp His Ala Gly Ser Glu Asp Ser Val Asp Ser Asp Glu Ser Asp 110
95 100 105 110

gaa tct cac cat tcg gat gag tct gat gag acc gtc act gct agt aca 447
Glu Ser His His Ser Asp Glu Ser Asp Glu Thr Val Thr Ala Ser Thr 125
115 120 125

caa gca gac act ttc act cca atc gtc cct aca gtc gat gtc ccc aac 495
Gln Ala Asp Thr Phe Thr Pro Ile Val Pro Thr Val Asp Val Pro Asn 140
130 135 140

ggc cga ggt gat agc ttg gct tat gga ctg agg tca aag tct agg agt 543
Gly Arg Gly Asp Ser Leu Ala Tyr Gly Leu Arg Ser Lys Ser Arg Ser 155
145 150 155

ttc cag gtt tct gat gaa cag tat cct gat gcc aca gat gag gac ctc 591
Phe Gln Val Ser Asp Glu Gln Tyr Pro Asp Ala Thr Asp Glu Asp Leu 170
160 165 170

acc tct cac atg aag agc ggt gag tct aag gag tcc ctc gat gtc atc 639
Thr Ser His Met Lys Ser Gly Glu Ser Lys Glu Ser Leu Asp Val Ile 190
175 180 185 190

cct gtt gcc cag ctt ctg agc atg ccc tct gat cag gac aac aac gga 687
Pro Val Ala Gln Leu Leu Ser Met Pro Ser Asp Gln Asp Asn Asn Gly 205
195 200 205

aag ggc agc cat gag tca agt cag ctg gat gaa cca agt ctg gaa aca 735
Lys Gly Ser His Glu Ser Ser Gln Leu Asp Glu Pro Ser Leu Glu Thr 220
210 215 220

cac aga ctt gag cat tcc aaa gag agc cag gag agt gcc gat cag tcg 783
His Arg Leu Glu His Ser Lys Glu Ser Gln Glu Ser Ala Asp Gln Ser 235
225 230 235

gat gtg atc gat agt caa gca agt tcc aaa gcc agc ctg gaa cat cag 831
Asp Val Ile Asp Ser Gln Ala Ser Ser Lys Ala Ser Leu Glu His Gln 250
240 245 250

agc cac aag ttt cac agc cac aag gac aag cta gtc cta gac cct aag 879
Ser His Lys Phe His Ser His Lys Asp Lys Leu Val Leu Asp Pro Lys 270
255 260 265 270

agt aag gaa gat gat agg tat ctg aaa ttc cga att tct cat gaa tta 927
 Ser Lys Glu Asp Asp Arg Tyr Leu Lys Phe Arg Ile Ser His Glu Leu 285
 275 280

gag agt tca tct tct gag gtc aac taa agaagaggca aaaacacagt 974
 Glu Ser Ser Ser Ser Glu Val Asn *
 290

tccttacttt gcatttagta aaaacaagaa aaagtgttag tgaggattaa gcaggaatac 1034
 taactgctca tttctcagtt cagtggatat atgtatgtag agaaagagag gtaatatattt 1094
 gggctcttag cttagtctgt tgtttcatgc aaacaaccgt tgtaaccaa agcttctgca 1154
 ctttgcttct gttcttcctg tacaagaaat gcaaacggcc actgcatttt aatgattggt 1214
 attcttttat gaataaaatg tatgtagaaa caagcaaatt tactgaaaca agcagaatta 1274
 aaagagaaac tgtaacagtc tatatcacta taccctttta gttttataat tagcatatat 1334
 tttgttgatga ttattttttt tgttggtgtg aataaatcctt gtaacgaatg t 1385

<210> 16
 <211> 294
 <212> PRT
 <213> mouse

<400> 16
 Met Arg Leu Ala Val Ile Cys Phe Cys Leu Phe Gly Ile Ala Ser Ser
 1 5 10 15
 Leu Pro Val Lys Val Thr Asp Ser Gly Ser Ser Glu Glu Lys Leu Tyr
 20 25 30
 Ser Leu His Pro Asp Pro Ile Ala Thr Trp Leu Val Pro Asp Pro Ser
 35 40 45
 Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu Glu
 50 55 60
 Lys Asp Asp Phe Lys Gln Glu Thr Leu Pro Ser Asn Ser Asn Glu Ser
 65 70 75 80
 His Asp His Met Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Gly Asp
 85 90 95
 His Ala Gly Ser Glu Asp Ser Val Asp Ser Asp Glu Ser Asp Glu Ser
 100 105 110
 His His Ser Asp Glu Ser Asp Glu Thr Val Thr Ala Ser Thr Gln Ala
 115 120 125
 Asp Thr Phe Thr Pro Ile Val Pro Thr Val Asp Val Pro Asn Gly Arg
 130 135 140
 Gly Asp Ser Leu Ala Tyr Gly Leu Arg Ser Lys Ser Arg Ser Phe Gln
 145 150 155 160
 Val Ser Asp Glu Gln Tyr Pro Asp Ala Thr Asp Glu Asp Leu Thr Ser
 165 170 175
 His Met Lys Ser Gly Glu Ser Lys Glu Ser Leu Asp Val Ile Pro Val
 180 185 190
 Ala Gln Leu Leu Ser Met Pro Ser Asp Gln Asp Asn Asn Gly Lys Gly
 195 200 205
 Ser His Glu Ser Ser Gln Leu Asp Glu Pro Ser Leu Glu Thr His Arg
 210 215 220
 Leu Glu His Ser Lys Glu Ser Gln Glu Ser Ala Asp Gln Ser Asp Val
 225 230 235 240
 Ile Asp Ser Gln Ala Ser Ser Lys Ala Ser Leu Glu His Gln Ser His
 245 250 255
 Lys Phe His Ser His Lys Asp Lys Leu Val Leu Asp Pro Lys Ser Lys
 260 265 270
 Glu Asp Asp Arg Tyr Leu Lys Phe Arg Ile Ser His Glu Leu Glu Ser
 275 280 285
 Ser Ser Ser Glu Val Asn
 290

<210> 17
 <211> 725
 <212> DNA
 <213> human

<220>

<221> CDS

<222> (54)...(353)

<400> 17

```
ctaaccacaga aacatccaat tctcaaactg aagctcgcac tctcgcctcc agc atg      56
                                         Met
                                         1

aaa gtc tct gcc gcc ctt ctg tgc ctg ctg ctc ata gca gcc acc ttc      104
Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr Phe
                    5                                10                    15

att ccc caa ggg ctc gct cag cca gat gca atc aat gcc cca gtc acc      152
Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val Thr
                    20                                25                    30

tgc tgt tat aac ttc acc aat agg aag atc tca gtg cag agg ctc gcg      200
Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala
                    35                                40                    45

agc tat aga aga atc acc agc agc aag tgt ccc aaa gaa gct gtg atc      248
Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile
                    50                                55                    60                    65

ttc aag acc att gtg gcc aag gag atc tgt gct gac ccc aag cag aag      296
Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys
                    70                                75                    80

tgg gtt cag gat tcc atg gac cac ctg gac aag caa acc caa act ccg      344
Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro
                    85                                90                    95

aag act tga acactcactc cacaacccaa gaatctgcag ctaacttatt      393
Lys Thr *
```

```
ttcccctagc tttcccacaga caccctgttt tattttatta taatgaattt tgtttgttga 453
tgtgaaacat tatgccttaa gtaatgttaa ttcttattta agttattgat gttttaagtt 513
tatctttcat ggtactagtg ttttttagat acagagactt ggggaaattg cttttcctct 573
tgaaccacag ttctacccct gggatgtttt gagggctctt gcaagaatca ttaatacaaa 633
gaattttttt taacattcca atgcattgct aaaatattat tgtggaaatg aatattttgt 693
aactattaca ccaaataaat atatttttgt ac                                725
```

<210> 18

<211> 99

<212> PRT

<213> human

<400> 18

```
Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
  1                    5                                10                    15
Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
                20                                25                    30
Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
    35                    40                    45
Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
    50                    55                    60
Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
    65                    70                    75                    80
Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
                85                                90                    95
Pro Lys Thr
```

<210> 19

<211> 584

<212> DNA

<213> mouse

[illegible]

```
<210> 20
<211> 148
<212> PRT
<213> mouse
```

<400>	20														
Met	Gln	Val	Pro	Val	Met	Leu	Leu	Gly	Leu	Leu	Phe	Thr	Val	Ala	Gly
1				5					10					15	
Trp	Ser	Ile	His	Val	Leu	Ala	Gln	Pro	Asp	Ala	Val	Asn	Ala	Pro	Leu
			20					25					30		
Thr	Cys	Cys	Tyr	Ser	Phe	Thr	Ser	Lys	Met	Ile	Pro	Met	Ser	Arg	Leu
		35					40					45			
Glu	Ser	Tyr	Lys	Arg	Ile	Thr	Ser	Ser	Arg	Cys	Pro	Lys	Glu	Ala	Val
	50					55					60				
Val	Phe	Val	Thr	Lys	Leu	Lys	Arg	Glu	Val	Cys	Ala	Asp	Pro	Lys	Lys
65					70					75					80
Glu	Trp	Val	Gln	Thr	Tyr	Ile	Lys	Asn	Leu	Asp	Arg	Asn	Gln	Met	Arg
				85					90					95	
Ser	Glu	Pro	Thr	Thr	Leu	Phe	Lys	Thr	Ala	Ser	Ala	Leu	Arg	Ser	Ser
			100					105					110		

Ala	Pro	Leu	Asn	Val	Lys	Leu	Thr	Arg	Lys	Ser	Glu	Ala	Asn	Ala	Ser
		115					120					125			
Thr	Thr	Phe	Ser	Thr	Thr	Thr	Ser	Ser	Thr	Ser	Val	Gly	Val	Thr	Ser
	130					135					140				
Val	Thr	Val	Asn												
145															